SEQUENCE LISTING

<110> Wang, Huaming
Bodie, Elizabeth A.

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<213> Stachybotrys chartarum

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Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
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225 230 235 240
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385 390 395 400
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Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His
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Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
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His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu
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Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys
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Glu Tyr Pro Leu Ile Phe Arg Gln Pro Leu Pro Ile Pro Pro Ala Lys
65                  70                  75                  80
Glu Pro Asn Lys Leu Thr Asn Pro Val Thr Asn Lys Glu Ile Trp Tyr
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Tyr Glu Ile Val Ile Lys Pro Phe Thr Gln Gln Val Tyr Pro Ser Leu
            100                 105                 110
Arg Pro Ala Arg Leu Val Gly Tyr Asp Gly Ile Ser Pro Gly Pro Thr
        115                 120                 125
Ile Ile Val Pro Arg Gly Thr Glu Ala Val Val Arg Phe Ile Asn Gln
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225                 230                 235                 240
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Replacement Sheet

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Ala Lys Val Pro Arg Gly Thr Val Glu Leu Trp Glu Leu Glu Asn Ser
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Ser Gly Gly Trp Ser His Pro Ile His Val His Leu Val Asp Phe Arg
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acaacagtga tggaactctc cagaccagtg tgggagaaga caacagtctc tggggcgacg 960
tcatccatgt caacggtcag ccctggccat tcttcaacgt tgagcctcga aagtatcgcc 1020
ttcgattcct caatgcggct gtttctcgga actttgccct ctatttcgtc aagcaacaag 1080
ccactgctac tagacttcct ttccaggtca ttgcctctga tgcagggcta ctcacgcacc 1140
cggtccaaac ctcagatatt tacgtggcag cagcagagcg ctacgagatt gtattcgact 1200
ttgcgcctta tgcaggccag acgatagatt tgcgtaactt tgcaaaggcc aatggggtcg 1260
gcaccgatga cgattatgca aacactgaca aggtcatgcg cttccatgtc agcagccaag 1320
cagtcgtcga taactcggtg gtacccgcac agctatctca gatccagttc cccgccgaca 1380
aaaccggcat cgaccaccac ttccgcttcc atcgcaccaa cagcgagtgg cgcatcaacg 1440
gcatcgggtt tgcagacgtc cagaaccgta tcctggccaa ggtaccgcgc ggcactgtcg 1500
agctatggga actcgagaac agctccggcg gctggtcgca ccccatccac gtccacctgg 1560
tcgacttccg agtcgtcgca cgctacggtg acgaaagcac tcgcggcgtc atgccctacg 1620
agtccgccgg tctcaaggac gtcgtgtggc tcggccgcca cgagacggtg ctcgtcgaag 1680
cacactacgc cccctgggac ggagtctaca tgttccactg ccacaacctg atccacgaag 1740
accaagacat gatggccgcg tttgacgtga ctaagctcca gaactttggc tacaacgaga 1800
cgacggattt ccacgacccg gaagattctc gctggtctgc aagacccttc accgcggctg 1860
acttgacggc gcgatcgggt atcttctcag aagcatccat cagggctaga gtgaacgagt 1920
tggcgctgga acagccgtac agcgaactgg cacaggtcac ggcctcgctc gagcagtact 1980
acaagacgaa caagaaacgc caggccgagt gcgaagacat gcctgctggc cccattcccc 2040

gttatcgcag gtttcaggtc tga 2063

<210> 7
<211> 627
<212> PRT
<213> Curvularia pallescens

<400> 7
Met Val Ala Lys Tyr Leu Phe Ser Ala Leu Gln Leu Ala Ser Ile Ala
1 5 10 15
Lys Gly Ile Tyr Gly Val Ala Leu Ser Glu Arg Pro Ala Lys Tyr Ile
20 25 30
Asp Glu Thr Pro Asp Glu Glu Lys Ala Ala Leu Ala Ala Ile Val Glu
35 40 45
Asp Asp Pro Ala Asp Val Phe Arg Ile Leu Lys Asp Trp Gln Ser Pro
50 55 60
Glu Tyr Pro Ile Leu Phe Arg Glu Ala Leu Pro Ile Pro Pro Ala Lys
65 70 75 80
Glu Pro Asn Lys Met Thr Asn Pro Val Thr Asn Lys Glu Ile Trp Tyr
85 90 95
Tyr Glu Ile Val Ile Lys Pro Phe Asn Gln Gln Val Tyr Pro Ser Leu
100 105 110
Arg Pro Ala Arg Leu Val Gly Tyr Asp Gly Ile Ser Pro Gly Pro Thr
115 120 125
Ile Ile Val Pro Arg Gly Thr Glu Ala Val Val Arg Phe Val Asn Gln
130 135 140
Gly Asp Arg Glu Ser Ser Ile His Leu His Gly Ser Pro Ser Arg Ala
145 150 155 160
Pro Phe Asp Gly Trp Ala Glu Asp Leu Ile Met Lys Gly Gln Phe Lys
165 170 175
Asp Tyr Tyr Tyr Pro Asn Asn Gln Ala Ala Arg Phe Leu Trp Tyr His
180 185 190
Asp His Ala Met His Val Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala
195 200 205
Gly Ala Tyr Leu Ile Thr Asp Pro Ala Glu Asp Ala Leu Gly Leu Pro
210 215 220
Ser Gly Tyr Gly Lys Tyr Asp Ile Pro Leu Val Leu Ser Ser Lys Phe
225 230 235 240
Tyr Asn Ser Asp Gly Thr Leu Gln Thr Ser Val Gly Glu Asp Asn Ser
245 250 255
Leu Trp Gly Asp Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Phe
260 265 270
Asn Val Glu Pro Arg Lys Tyr Arg Leu Arg Phe Leu Asn Ala Ala Val
275 280 285
Ser Arg Asn Phe Ala Leu Tyr Phe Val Lys Gln Gln Ala Thr Ala Thr
290 295 300
Arg Leu Pro Phe Gln Val Ile Ala Ser Asp Ala Gly Leu Leu Thr His
305 310 315 320
Pro Val Gln Thr Ser Asp Ile Tyr Val Ala Ala Ala Glu Arg Tyr Glu
325 330 335
Ile Val Phe Asp Phe Ala Pro Tyr Ala Gly Gln Thr Ile Asp Leu Arg
340 345 350
Asn Phe Ala Lys Ala Asn Gly Val Gly Thr Asp Asp Asp Tyr Ala Asn
355 360 365
Thr Asp Lys Val Met Arg Phe His Val Ser Ser Gln Ala Val Val Asp
370 375 380
Asn Ser Val Val Pro Ala Gln Leu Ser Gln Ile Gln Phe Pro Ala Asp

```
385                 390                 395                 400
Lys Thr Gly Ile Asp His His Phe Arg Phe His Arg Thr Asn Ser Glu
                405                 410                 415
Trp Arg Ile Asn Gly Ile Gly Phe Ala Asp Val Gln Asn Arg Ile Leu
            420                 425                 430
Ala Lys Val Pro Arg Gly Thr Val Glu Leu Trp Glu Leu Glu Asn Ser
        435                 440                 445
Ser Gly Gly Trp Ser His Pro Ile His Val His Leu Val Asp Phe Arg
    450                 455                 460
Val Val Ala Arg Tyr Gly Asp Glu Ser Thr Arg Gly Val Met Pro Tyr
465                 470                 475                 480
Glu Ser Ala Gly Leu Lys Asp Val Val Trp Leu Gly Arg His Glu Thr
                485                 490                 495
Val Leu Val Glu Ala His Tyr Ala Pro Trp Asp Gly Val Tyr Met Phe
            500                 505                 510
His Cys His Asn Leu Ile His Glu Asp Gln Asp Met Met Ala Ala Phe
        515                 520                 525
Asp Val Thr Lys Leu Gln Asn Phe Gly Tyr Asn Glu Thr Thr Asp Phe
    530                 535                 540
His Asp Pro Glu Asp Ser Arg Trp Ser Ala Arg Pro Phe Thr Ala Ala
545                 550                 555                 560
Asp Leu Thr Ala Arg Ser Gly Ile Phe Ser Glu Ala Ser Ile Arg Ala
                565                 570                 575
Arg Val Asn Glu Leu Ala Leu Glu Gln Pro Tyr Ser Glu Leu Ala Gln
            580                 585                 590
Val Thr Ala Ser Leu Glu Gln Tyr Tyr Lys Thr Asn Lys Lys Arg Gln
        595                 600                 605
Ala Glu Cys Glu Asp Met Pro Ala Gly Pro Ile Pro Arg Tyr Arg Arg
    610                 615                 620
Phe Gln Val
625
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<210> 8
<211> 858
<212> DNA
<213> Amerosporium atrum

<220>
<221> misc_feature
<222> (1)...(858)
<223> n = A,T,C or G

<400> 8

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caccgccgag aacgcttact ttggtcaagc tggcttttac attctgcacg accccgctga      60
agatgcattg ggtctgcctt ctggcaagta tgatgtacct cttgcactgt cctccaagca     120
gtacaacagc gacggtaccc tcttcgaccc caaggacgag accgattcac tgttcggcga     180
tgtcatccac gtcaacggac agccatggcc ctactttaag gtcgagcctc gcaagtaccg     240
tctccgcttc ctcaatgctg ctatcagccg tgccttcaag ctcactttcg aggctgatgg     300
caaagtgatc aactttcctg tcatcggtgc cgatactggt ctcttgacca agcctgttca     360
gacaagcaac cttgagatct ctatggccga gcgctgggag gttgtttttg acttcagcca     420
attttccggg aagaacgtca ccctcaagaa cggtcgcgat gtgcagcacg atgaggacta     480
caactccacc gacaaagtca tgcagttcgt tgttggcaag gatgttacga gccaggctgg     540
taatggcaac cttcccggct ctctgcgcac tgttcccttc cctcctaaga aggggcggag     600
tcgacaggag cttcaagttc ggcagggacc ggtggccagt ggactgttaa tggcttgacc     660
ttcgctgatg tcaacaaccg catcctggct aagcccccaa cgtggtgcca tcgaggtttt     720
gggagctttg agaacttcca gcggnggntg gtcttaccct tgtccacatc cacctgggtc     780
gactttccag atncttgtct tgcactggan gcaaggcncc ccgttntaac tncnanaaag     840
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gaagcacttt caagggcg 858

<210> 9
<211> 114
<212> PRT
<213> Amerosporium atrum

<220>
<221> VARIANT
<222> (1)...(114)
<223> Xaa = space of unknown number of aa

<400> 9
Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Phe Tyr Ile Leu His
1 5 10 15
Asp Pro Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Lys Tyr Asp Val
20 25 30
Pro Leu Ala Leu Ser Leu Lys Ala Tyr Asn Ser Asp Gly Thr Leu Phe
35 40 45
Asp Pro Lys Asp Glu Thr Asp Ser Leu Phe Gly Asp Val Ile His Val
50 55 60
Asn Gly Gln Pro Trp Pro Tyr Leu Lys Val Glu Pro Arg Lys Tyr Arg
65 70 75 80
Leu Arg Phe Leu Asn Ala Ala Ile Ser Arg Ala Phe Lys Xaa Val Trp
85 90 95
Glu Leu Glu Asn Thr Ser Ser Gly Gly Trp Ser Tyr Pro Val His Ile
100 105 110
His Leu

<210> 10
<211> 19
<212> PRT
<213> Stachybotrys chartarum

<220>
<221> VARIANT
<222> (1)...(19)
<223> Xaa = Any Amino Acid

<400> 10
Asp Tyr Tyr Phe Pro Asn Tyr Gln Ser Ala Arg Leu Leu Xaa Tyr His
1 5 10 15
Asp His Ala

<210> 11
<211> 13
<212> PRT
<213> Stachybotrys chartarum

<400> 11
Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
1 5 10

<210> 12
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> degenerated primer

<221> misc_feature
<222> (12)...(12)
<223> n = A,T,C or G

<221> misc_feature
<222> (15)...(20)
<223> n = T or C

<400> 12
tattactttc cnaantanca 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerated primer

<221> misc_feature
<222> (1)...(20)
<223> n = A,T,C or G

<400> 13
tcgtatggca tnacctgncc 20

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(20)
<223> n = T or C

<400> 14
tggtaccang ancangct 18

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(1)

<223> n = A or G

<221> misc_feature
<222> (10)...(10)
<223> n = T or G

<400> 15
ngactcgtan ggcatgac 18

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(21)
<223> n = A or G

<400> 16
tcgtggatga nnttgtgnca n 21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (2)...(2)
<223> n = A,T,C or G

<221> misc_feature
<222> (5)...(10)
<223> n = A or G

<221> misc_feature
<222> (13)...(13)
<223> n = T or C

<221> misc_feature
<222> (15)...(15)
<223> n = A or G

<400> 17
cnagacnacn tcnttnagac c 21

Replacement Sheet